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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
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GREENLEE WINNER AND SULLIVAN P C
4875 PEARL EAST CIRCLE
SUITE 200
BOULDER, CO 80301

EXAMINER	
MEHTA, ASHWIN D	

ART UNIT	PAPER NUMBER
1638	

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Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	10/049,137	OGAS ET AL.	
	Examiner	Art Unit	
	Ashwin Mehta	1638	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *15 April 2005*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-84* is/are pending in the application.

4a) Of the above claim(s) *38-54,76 and 80-84* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-37,55-75 and 77-79* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☒ The specification is objected to by the Examiner.

10)☒ The drawing(s) filed on *30 June 2002* is/are: a)☒ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☒ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☒ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☒ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date *9302002*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____.
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☐ Other: _____.

DETAILED ACTION

Election/Restrictions

1. Applicant's election with traverse of Group I, claims 1-37, 55-75, and 77-79 in the reply filed on April 15, 2005 is acknowledged. The traversal is on the ground(s) that Groups I and II are linked in that they take advantage of the particular coding sequences related to developmental regulation; that Groups I and II use the sense and antisense of the sequences; and that Group III relates to the protein encoded by the coding sequence of the invention (response, page 2, 3rd full paragraph). This is not found persuasive because the method of Group III will not produce the same effect in the host as the method of Group I, since different sequences are being expressed. Group I also comprises using nucleotide sequences that do not encode the proteins encompassed by the claims of Group III.

The requirement is still deemed proper and is therefore made FINAL. Non-elected claims 38-54 and 80-83 are withdrawn from consideration.

Claim Objections

3. Claim 15, 63, 67, and 68 are objected to for the following reasons:

In claim 15: the claim is objected to under 37 CFR 1.75(c), as being of improper dependent form for failing to further limit the subject matter of a previous claim. Applicant is required to cancel the claim(s), or amend the claim(s) to place the claim(s) in proper dependent form, or rewrite the claim(s) in independent form. Claim 15 attempts to limit the method of claim 1 by requiring deletion of the nucleotide sequences encoding one of the domains.

However, the method of claim 1 does not encompass any such nucleotide sequence. A method wherein the nucleic acid molecule does not encode one of the domains would infringe claim 15, but not claim 1, which requires all of the recited domains to be present.

In claims 63, 67, and 68: the claims are missing the period punctuation mark.

Appropriate correction is required.

Specification

4. The disclosure is objected to because it contains an embedded hyperlink and/or other form of browser-executable code, for example on page 25, lines 20 and 30, and page 26, line 21. Applicant is required to delete the embedded hyperlink and/or other form of browser-executable code. See MPEP § 608.01.

Claim Rejections - 35 USC § 112

The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

5. Claims 2, 3, 5, 6, 8, 9, 16-18, 24, 25, 61, 63-69, and 78 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

In claim 2: the recitation, "wherein said nucleic acid molecule further encodes a protein having at least one zinc finger domain" renders the claim indefinite. It is unclear if the recitation is attempting to limit the protein mentioned in claim 1, or if it is indicating that the nucleic acid molecule encodes a second, distinct protein.

In claim 16: the recitation, "wherein said protein has a point mutation in lysine 304" renders the claim indefinite. There is no indication in claim 16, or parent claim 1, that the amino acid in position 304 of the protein is a lysine. Further, there is no indication that the protein encoded by the nucleic acid molecule even has 304 amino acids. It is unclear if the claim is attempting to limit claim 1 by requiring the protein to have at least 304 amino acids. The recitation could also indicate that a specific amino acid sequence is being referred to. However, it is unclear what this sequence is. The metes and bounds of the claim are unclear.

In claims 18, 24, 61, 78: the recitation, "PKL" renders the claims indefinite. Page 10 of the specification indicates that "PKL" refers generally to any protein described therein, and to any variants which function in regulating developmental identity. This definition does not distinguish a protein as a "PKL", as it encompasses all proteins involved in regulating developmental identity, which have different functions, and effect development in distinct manners.

In claim 24: there is insufficient antecedent basis in the claim, or parent claim 1, for the limitations, "said PKL", and "said plant".

In claim 25: the recitation, "substantial similarity" renders the claim indefinite. The recitation is relative, and has not definite meaning. It is unclear when a sequence does not have substantial similarity to the nucleotide sequence of SEQ ID NO: 1. The metes and bounds of the claim are unclear.

In claim 63: the recitation, "said nucleotide" in the last line renders the claim indefinite. It is unclear what nucleotide the recitation is referring to.

In claims 67 and 68: the claims are indefinite because they are incomplete. Claims 67-69 , cannot be further examined on the merits.

In claim 78: the recitation, "wherein said protein has the amino acid sequence of PKL" renders the claim indefinite. The recitation is referring to a particular amino acid sequence. However, it is unclear what this sequence is.

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

6. Claims 1-18, 20-27, 30-37, 55-61, 63-65, 70, 71, and 73-75 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

The claims are broadly drawn towards a method of transforming any host cell, comprising introduction of any nucleic acid molecule encoding any protein having at least one chromo domain, a helicase domain, and a DNA binding domain, said protein expressed in an amount sufficient to regulate developmental identity; or wherein said nucleic acid molecule further encodes a protein having at least one zinc finger domain; or wherein said nucleic acid molecule further encodes a second chromo domain; or where said chromo domain is encoded by a nucleotide sequence having at least 50% identity to bases 343-453 of SEQ ID NO: 1, said helicase domain is encoded by a sequence having at least 50% identity to bases 877-2217 of SEQ

ID NO: 1, and said DNA binding domain is encoded by a sequence having at least 50% identity to bases 3205-3285 of SEQ ID NO: 1; or wherein said zinc finger is encoded by a sequence having at least 50 % identity to bases 145-288 of SEQ ID NO: 1; or wherein the second chromo domain is encoded by a sequence having at least 50% identity to bases 571-681 of SEQ ID NO: 1; or wherein said chromo, helicase, DNA binding, zinc finger, and second chromo domains have at least 50% identity to residues 115-151, 293-739, 1069-1095, 49-96, and 191-227, respectively, of SEQ ID NO: 2; or wherein said protein has a point mutation at lysine 304; or wherein said protein encodes any PKL; or wherein said nucleic acid molecule comprises a sequence having substantial similarity to SEQ ID NO: 1; or a method of transforming any host cell comprising introduction of any amino acid sequence having at least 50% identity to SEQ ID NO: 2 and functioning in regulating developmental identity; or a recombinant nucleic acid molecule comprising a sequence encoding any protein having at least one chromo domain, a helicase domain, and a DNA binding domain, said protein expressed in an amount sufficient to regulate developmental identity, and a foreign promoter operably linked to said sequence; or wherein said nucleic acid molecule further encodes a protein having at least one zinc finger domain.

The specification indicates that amino acid sequence of an Arabidopsis thaliana protein termed PKL ("PICKLE") is set forth in SEQ ID NO: 2, and is encoded by the nucleotide sequence of SEQ ID NO: 1 (page 10, lines 13-15). The specification indicates that this PKL encodes for a "CHD3" homolog (page 32, lines 16-17). CHD proteins have three domains, a chromo domain (chromatin organization modifier), a SNF2-related helicase domain, and a DNA binding domain. CHD3 proteins are distinguished from CHD1 proteins by the presence of a

PHD zinc finger domain (page 32, lines 27-31). CHD3 proteins are thought to be involved in transcription repression, and the PKL of SEQ ID NO: 2 is necessary to repress embryonic identity in A. thaliana. The specification admits that there is little published evidence of the function of CHD1 proteins (pages 36-39).

However, the specification does not teach any and all nucleotide sequences encoding a protein having at least one chromo domain, a helicase domain, and a DNA binding domain that regulates developmental identity in any cell. As discussed above, the specification indicates that proteins having this combination of domains are referred to as CHD proteins, and those lacking a zinc finger domain are classified as CHD1 proteins. The specification also admits that there is little published evidence of the function of CHD1 proteins. The specification does not describe any CHD1 proteins that effect developmental identity of any and all host cells. See Amgen Inc. v. Chugai Pharmaceutical Co. Ltd., 18 USPQ2d 1016 at 1021 and 1027, (Fed. Cir. 1991) at page 1021, where it is taught that a gene is not reduced to practice until the inventor can define it by "its physical or chemical properties" (e.g. a DNA sequence).

As discussed above, the specification indicates the SEQ ID NO: 2 is an A. thaliana protein termed PKL, that it is categorized as a CHD3 protein because of the presence of a zinc finger domain, and that it is involved in repressing embryonic traits in A. thaliana seedlings. However, the specification does not describe any nucleotide sequences that encode proteins that differ from SEQ ID NO: 2 and which retain its transcription repressing activity and repress embryonic traits in seedlings. The specification does not describe the sequences of the domains of SEQ ID NO: 2 that can be changed without affecting their activities. The Federal Circuit provided the appropriate standard for written description in University of California v. Eli Lilly

& Co. 119 F.3d 1559, 43 USPQ2d 1398 (Fed. Cir. 1997). The court held that a structural description of a rat cDNA was not an adequate description of broader classes of cDNAs, because a "written description of an invention involving a chemical genus, like a description of a chemical species, requires a precise definition, such as by structure, formula, [or] chemical name, of the claimed subjected matter sufficient to distinguish it from other materials. The only nucleotide sequences that are correlated with the activity of repressing embryonic traits in A. thaliana seedlings are those encoding SEQ ID NO: 2. Further, the claims broadly encompass regulating developmental identity in any manner, in any host cell of any species. The specification does not describe other function for SEQ ID NO: 2 other than repressing embryonic traits in seedlings. The specification does not describe any nucleotide sequence comprising sequences that have at least 50% identity to bases 343-453, 877-2217, 3205-3285, and 145-288 of SEQ ID NO: 1, or which encode an amino acid sequence having domains that have at least 50% identity to residues 115-151, 293-739, 1069-1095, 49-96, and 191-227 of SEQ ID NO: 2, or at least 50% identity to SEQ ID NO: 1 or encoding a protein having at least 50% identity to SEQ ID NO: 2, that regulate developmental identity in any manner in any and all host cell types. The specification further does not describe a single protein having chromo, helicase, and DNA-binding domains, and further having a point mutation at a lysine 304, that regulates developmental identity in any manner in any and all host cell types. Given the breadth of the claims, it is submitted that the specification fails to provide an adequate written description of the multitude of nucleic acid sequences encompassed by the claims.

7. Claims 1-37, 55-66, 70-75, and 77-79 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for a recombinant nucleic acid molecule comprising SEQ ID NO: 1 or sequences differing from it due to genetic code degeneracy, does not reasonably provide enablement for a method of transforming any and all host cells with a nucleic acid molecule encoding a protein having at least one chromo domain, a helicase domain, and a DNA binding domain, or further comprising a zinc finger domain, wherein the protein regulates developmental identity in any manner; or encoding a protein with a point mutation at lysine 304; any other recombinant nucleic acid molecule; eukaryotic cells or transgenic plants comprising a nucleic acid molecule having a protein functioning in regulating developmental identity in any manner and having at least 50% identity to SEQ ID NO: 2. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention commensurate in scope with these claims.

The claims are broadly drawn towards a method of transforming any host cell, comprising introduction of any nucleic acid molecule encoding any protein having at least one chromo domain, a helicase domain, and a DNA binding domain, said protein expressed in an amount sufficient to regulate developmental identity; or wherein said nucleic acid molecule further encodes a protein having at least one zinc finger domain; or wherein said nucleic acid molecule further encodes a second chromo domain; or where said chromo domain is encoded by a nucleotide sequence having at least 50% identity to bases 343-453 of SEQ ID NO: 1, said helicase domain is encoded by a sequence having at least 50% identity to bases 877-2217 of SEQ ID NO: 1, and said DNA binding domain is encoded by a sequence having at least 50% identity to bases 3205-3285 of SEQ ID NO: 1; or wherein said zinc finger is encoded by a sequence

having at least 50 % identity to bases 145-288 of SEQ ID NO: 1; or wherein the second chromo domain is encoded by a sequence having at least 50% identity to bases 571-681 of SEQ ID NO: 1; or wherein said chromo, helicase, DNA binding, zinc finger, and second chromo domains have at least 50% identity to residues 115-151, 293-739, 1069-1095, 49-96, and 191-227, respectively, of SEQ ID NO: 2; or wherein said protein has a point mutation at lysine 304; or wherein said protein encodes any PKL; or wherein said nucleic acid molecule comprises a sequence having substantial similarity to SEQ ID NO: 1; or a method of transforming any host cell comprising introduction of any amino acid sequence having at least 50% identity to SEQ ID NO: 2 and functioning in regulating developmental identity; or a recombinant nucleic acid molecule comprising a sequence encoding any protein having at least one chromo domain, a helicase domain, and a DNA binding domain, said protein expressed in an amount sufficient to regulate developmental identity, and a foreign promoter operably linked to said sequence; or wherein said nucleic acid molecule further encodes a protein having at least one zinc finger domain.

The specification indicates that amino acid sequence of an Arabidopsis thaliana protein termed PKL ("PICKLE") is set forth in SEQ ID NO: 2, and is encoded by the nucleotide sequence of SEQ ID NO: 1 (page 10, lines 13-15). The specification indicates that this PKL encodes for a "CHD3" homolog (page 32, lines 16-17). CHD proteins have three domains, a chromo domain (chromatin organization modifier), an SNF2-related helicase domain, and a DNA binding domain. CHD3 proteins are distinguished from CHD1 proteins by the presence of a PHD zinc finger domain (page 32, lines 27-31). CHD3 proteins are thought to be involved in transcription repression, and the PKL of SEQ ID NO: 2 is necessary to repress embryonic

identity in A. thaliana. The specification admits that there is little published evidence of the function of CHD1 proteins (pages 36-39).

The specification does not enable nucleotide sequences encoding a protein functioning in regulating developmental identity, wherein the protein has at least one chromo domain, helicase domain, and DNA binding domain. As discussed, such proteins are categorized as CHD1 proteins, and the specification admits that there was little evidence of their function at the time of filing. In the absence of further guidance, undue experimentation would be required by one skilled in the art to determine their function. The specification discusses SEQ ID NO: 2, and A. thaliana pkl mutant plants. However, the specification does not teach any CHD1 genes involved in regulating developmental identity in any manner, of any cell. See Genentech, Inc. v. Novo Nordisk, A/S, 42 USPQ2d 1001, 1005 (Fed. Cir. 1997), which teaches that "the specification, not the knowledge of one skilled in the art" must supply the enabling aspects of the invention.

The specification also does not teach any nucleic acid molecules encoding a protein having a chromo domain, helicase domain, DNA binding domain, and a zinc finger domain, that has at least 50% identity to bases 343-453, 877-2217, 3205-3285, and 145-288 of SEQ ID NO: 1, or which encode an amino acid sequence having domains that have at least 50% identity to residues 115-151, 293-739, 1069-1095, 49-96, and 191-227 of SEQ ID NO: 2, or at least 50% identical to SEQ ID NO: 1 or encoding a protein having at least 50% identity to SEQ ID NO: 2, that retain the activity of SEQ ID NO: 2, other than SEQ ID NO: 1 and nucleotide sequences that differ therefrom by genetic code degeneracy. The specification does not teach how the sequences of any of the domains of SEQ ID NO: 2, or any other sequence within SEQ ID NO: 2, may differ without altering its functional activity. Guo et al. (PNAS, 2004, Vol. 101, pages

9205-9210) quantitate a protein's tolerance to random change, and defined the probability that a random amino acid change will lead to functional inactivation as the "x factor." Guo et al. teach that the x factor for the human AAG gene is 34%, and found that diverse proteins have a similar range of x factors (pages 9206-9207). The nucleotide sequences encompassed by the claims differ from SEQ ID NO: 1 by as much as 50%, or encode proteins that differ from SEQ ID NO: 2 in as much as 50%. In the absence of further guidance, undue experimentation would be required by one skilled in the art to determine what amino acids of SEQ ID NO: 2 may be changed, and what to change them to, without altering functional activity.

Further, the specification does not teach that developmental identity was regulated in any manner, in any host cell, as encompassed by the claimed methods. As discussed above, the specification indicates that in Arabidopsis mutant pkl plants, embryonic traits are expressed after seed germination. The specification indicates on page 22, lines 16-17, that the methods may be used to promote the transition from embryonic to post-embryonic state. However, the specification does not show that transgenic plants overexpressing SEQ ID NO: 1 or any other nucleic acid molecule encompassed by the claims actually caused such a phenotype. Larkin et al (1994, The Plant Cell 6:1065-1076) teach the unpredictability of transforming a plant to produce the opposite phenotype as the mutant-gene phenotype. Larkin et al teach that *GLABROUS1* (*GL1*) mutant plants have a reduced number of trichomes. However, overexpressing GL1 in *Arabidopsis* did not produce plants with an increased number of trichomes compared to wild-type plants (page 1072). In the instant case, one skilled in the art would not just conclude that overexpression of SEQ ID NO: 1 would promote the embryonic to post-embryonic transition of plants. Further, that SEQ ID NO: 2 is a transcriptional repressor brings up the question of

whether the repression of genes required for embryonic development, during the time of embryonic development itself, would allow the transgenic host to be viable. The claims also broadly encompass any type of regulation of developmental identity. However, the specification does not teach any other manner of involvement of SEQ ID NO: 2 in developmental identity. Undue experimentation would be required by one skilled in the art to determine the effect of overexpressing SEQ ID NO: 1 or any other nucleotide sequence in any transgenic plant, plant cell, or other host cell.

The claims also broadly encompass transforming any host cell of any species. However, as SEQ ID NO: 2 is a plant protein, it is unclear that its expression would affect the developmental identity of any and all host cells of all species in any manner. Ogas et al. (PNAS, 1999, Vol. 96, pages 13838-13844) teach that it remains to be determined whether CHD proteins in animal systems will play an analogous role as the Arabidopsis PKL in hormone-related developmental events (page 13844). In light of this teaching, undue experimentation would be required by one skilled in the art to determine what developmental events would be affected by the claimed methods, if at all.

Further, regarding claims 16-17: the specification indicates on page 42, lines 13-19 that the prior art teaches that a point mutation of a conserved lysine in the ATPase/helicase domain of SWI/SNF proteins generates a dominant negative protein. The specification cites Khavari et al. (Nature, 1996, Vol. 366, pages 170-174), which teaches that mutant yeast SWI and human BRGI proteins, with lysine to arginine mutations at lysine 798 and 783, respectively, abolished their transcription activation activity of certain promoters, but not of others (page 173). However, these proteins are transcriptional activators, and Khavari et al. teach that the inactivation of the

mutants is due to formation of nonfunctional activator complexes at specific promoter sites (page 173). Instant SEQ ID NO: 2, on the other hand, is a CHD3 protein, which are transcriptional repressors. The specification teaches that CHD3 proteins are part of a complex that contains a histone deacetylase, and deacetylation of histones is correlated with transcriptional activation (page 27, line 39 to page 38, line 5). As the proteins taught by Khavari et al., and SEQ ID NO: 2 are distinct and have different activities and mechanisms of action, undue experimentation would be required by one skilled in the art to mutate the conserved lysine residue taught by Khavari et al., in SEQ ID NO: 2 or any other sequence encompassed by the claims, to generate a dominant negative mutant protein. Example 4 in the specification is prophetic and does not show that a dominant negative mutant was made. Given the breadth of the claims, unpredictability of the art and lack of guidance of the specification as discussed above, undue experimentation would be required by one skilled in the art to make and use the claimed invention.

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

8. Claims 1-3, 10, 18, 21-23, and 55-57 are rejected under 35 U.S.C. 102(b) as being anticipated by Woodage et al. (PNAS, 1997, Vol. 94, pages 11472-11477).

Woodage et al teach the characterization of CHD family of proteins. Numerous proteins having chromo domains, helicase domains, and DNA binding domains are taught, for example

the murine CHDI protein, and the gene that encodes it. The λZAPII expression system was used to clone cDNAs (pages 11472-11474). CHD proteins that further contain a zinc finger domain and/or a second chromo domain are also taught, for example HsCHDS (pages l 1473 and l 1475). Yeast strains transformed with ScCHD1 are also taught (page l 1473). The proteins encoded by the nucleotide sequences taught by Woodage et al. can be considered to be "PKL" proteins, given the open-ended and ambiguous definition of PKL in the instant specification, as discussed above.

9. None-elected claims 38-54, 76, and 80-84 are withdrawn from consideration and claims 1-37, 55-75, and 77-79 are rejected.

Contact Information

Any inquiry concerning this or earlier communications from the Examiner should be directed to Ashwin Mehta, whose telephone number is 571-272-0803. The Examiner can normally be reached from 8:00 A.M to 5:30 P.M. If attempts to reach the Examiner by telephone are unsuccessful, the Examiner's supervisor, Amy Nelson, can be reached at 571-272-0804. The fax phone numbers for the organization where this application or proceeding is assigned are 571-273-8300. Patent applicants with problems or questions regarding electronic images that can be viewed in the Patent Application Information Retrieval system (PAIR) can now contact the USPTO's Patent Electronic Business Center (Patent EBC) for assistance. Representatives are available to answer your questions daily from 6 am to midnight (EST). The toll free number is (866) 217-9197. When calling please have your application serial or patent number, the type of document you are having an image problem with, the number of pages and the specific nature of the problem. The Patent Electronic Business Center will notify applicants of the resolution of the problem within 5-7 business days. Applicants can also check PAIR to confirm that the problem has been corrected. The USPTO's Patent Electronic Business Center is a complete service center supporting all patent business on the Internet. The USPTO's PAIR system provides Internet-based access to patent application status and history information. It also enables applicants to view the scanned images of their own application file folder(s) as well as general patent information available to the public. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished

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June 22, 2005

Ashwin D. Mehta, Ph.D.
Primary Examiner
Art Unit 1638